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1638

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304A

DATE: 07/07/2000
TIME: 02:21:49

INPUT SET: S35672.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: EPELBAUM, SABINE URSULA
6 FALCO, SAVERIO CARL
7 MCDEVITT, RAYMOND ERVIN, III
8
9 (ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
10 INCREASING THE LYSINE CONTENT OF
11 THE SEEDS OF PLANTS
12
13 (iii) NUMBER OF SEQUENCES: 132
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
17 (B) STREET: 1007 MARKET STREET
18 (C) CITY: WILMINGTON
19 (D) STATE: DELAWARE
20 (E) COUNTRY: U.S.A.
21 (F) ZIP: 19898
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
25 (B) COMPUTER: IBM PC COMPATIBLE
26 (C) OPERATING SYSTEM: MICROSOFT OFFICE 97
27 (D) SOFTWARE: MICROSOFT WINDOWS 95
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/824,627
36 (B) FILING DATE: MARCH 27, 1997
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: CHRISTENBURY, LYNNE M.
40 (B) REGISTRATION NUMBER: 30,971
41 (C) REFERENCE/DOCKET NUMBER: BB-1037-F
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: 302-992-5481
45 (B) TELEFAX: 302-892-7949
46 (C) TELEX: 835420

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RAW SEQUENCE LISTING
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47
 48
 49
 50 (2) INFORMATION FOR SEQ ID NO:1:
 51
 52 (i) SEQUENCE CHARACTERISTICS:
 53 (A) LENGTH: 1350 base pairs
 54 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: single
 56 (D) TOPOLOGY: linear
 57
 58 (ii) MOLECULE TYPE: DNA (genomic)
 59
 60 (ix) FEATURE:
 61 (A) NAME/KEY: CDS
 62 (B) LOCATION: 1..1350
 63
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 65
 66 ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT 48
 67 Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
 68 1 5 10 15
 69
 70 TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC 96
 71 Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
 72 20 25 30
 73
 74 GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG 144
 75 Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
 76 35 40 45
 77
 78 GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC 192
 79 Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
 80 50 55 60
 81
 82 GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC 240
 83 Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
 84 65 70 75 80
 85
 86 CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT 288
 87 Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
 88 85 90 95
 89
 90 GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT 336
 91 Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
 92 100 105 110
 93
 94 GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG 384
 95 Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
 96 115 120 125
 97
 98 ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA 432
 99 Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys

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100	130	135	140	
101				
102	GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC			480
103	Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala			
104	145	150	155	160
105				
106	GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA			528
107	Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu			
108		165	170	175
109				
110	GGC TTA GTG ATC ACC CAG GGA TTT ATC GGT AGC GAA AAT AAA GGT CGT			576
111	Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg			
112		180	185	190
113				
114	ACA ACG ACG CTT GGC CGT GGA GGC AGC GAT TAT ACG GCA GCC TTG CTG			624
115	Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu			
116		195	200	205
117				
118	GCG GAG GCT TTA CAC GCA TCT CGT GTT GAT ATC TGG ACC GAC GTC CCG			672
119	Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro			
120		210	215	220
121				
122	GGC ATC TAC ACC ACC GAT CCA CGC GTA GTT TCC GCA GCA AAA CGC ATT			720
123	Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile			
124		225	230	235
125				240
126	GAT GAA ATC GCG TTT GCC GAA GCG GCA GAG ATG GCA ACT TTT GGT GCA			768
127	Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala			
128		245	250	255
129				
130	AAA GTA CTG CAT CCG GCA ACG TTG CTA CCC GCA GTA CGC AGC GAT ATC			816
131	Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile			
132		260	265	270
133				
134	CCG GTC TTT GTC GGC TCC AGC AAA GAC CCA CGC GCA GGT GGT ACG CTG			864
135	Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu			
136		275	280	285
137				
138	GTG TGC AAT AAA ACT GAA AAT CCG CCG CTG TTC CGC GCT CTG GCG CTT			912
139	Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu			
140		290	295	300
141				
142	CGT CGC AAT CAG ACT CTG CTC ACT TTG CAC AGC CTG AAT ATG CTG CAT			960
143	Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His			
144		305	310	315
145				320
146	TCT CGC GGT TTC CTC GCG GAA GTT TTC GGC ATC CTC GCG CGG CAT AAT			1008
147	Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn			
148		325	330	335
149				
150	ATT TCG GTA GAC TTA ATC ACC ACG TCA GAA GTG AGC GTG GCA TTA ACC			1056
151	Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr			
152		340	345	350

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153
154   CTT GAT ACC ACC GGT TCA ACC TCC ACT GGC GAT ACG TTG CTG ACG CAA 1104
155   Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
156           355                               360 ----- 365
157
158   TCT CTG CTG ATG GAG CTT TCC GCA CTG TGT CGG GTG GAG GTG GAA GAA 1152
159   Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
160           370                               375                               380
161
162   GGT CTG GCG CTG GTC GCG TTG ATT GGC AAT GAC CTG TCA AAA GCC TGC 1200
163   Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
164   385                               390                               395                               400
165
166   GCC GTT GGC AAA GAG GTA TTC GGC GTA CTG GAA CCG TTC AAC ATT CGC 1248
167   Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
168           405                               410                               415
169
170   ATG ATT TGT TAT GGC GCA TCC AGC CAT AAC CTG TGC TTC CTG GTG CCC 1296
171   Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
172           420                               425                               430
173
174   GGC GAA GAT GCC GAG CAG GTG GTG CAA AAA CTG CAT AGT AAT TTG TTT 1344
175   Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
176           435                               440                               445
177
178   GAG TAA
179   Glu *
180           450
181
182   (2) INFORMATION FOR SEQ ID NO:2:
183
184   (i) SEQUENCE CHARACTERISTICS:
185   (A) LENGTH: 36 base pairs
186   (B) TYPE: nucleic acid
187   (C) STRANDEDNESS: single
188   (D) TOPOLOGY: linear
189
190   (ii) MOLECULE TYPE: DNA (genomic)
191
192   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
193
194   GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG 36
195
196   (2) INFORMATION FOR SEQ ID NO:3:
197
198   (i) SEQUENCE CHARACTERISTICS:
199   (A) LENGTH: 36 base pairs
200   (B) TYPE: nucleic acid
201   (C) STRANDEDNESS: single
202   (D) TOPOLOGY: linear
203
204   (ii) MOLECULE TYPE: DNA (genomic)
205
    
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206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
207
208 GTACCGCCAA ATTTGGAGAC AACAAATTCA GCCATG 36
209
210 (2) INFORMATION FOR SEQ ID NO:4:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 48 base pairs
214 (B) TYPE: nucleic acid
215 (C) STRANDEDNESS: single
216 (D) TOPOLOGY: linear
217
218 (ii) MOLECULE TYPE: DNA (genomic)
219
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
221
222 CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT 48
223
224 (2) INFORMATION FOR SEQ ID NO:5:
225
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 37 base pairs
228 (B) TYPE: nucleic acid
229 (C) STRANDEDNESS: single
230 (D) TOPOLOGY: linear
231
232 (ii) MOLECULE TYPE: DNA (genomic)
233
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
235
236 GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTC 37
237
238 (2) INFORMATION FOR SEQ ID NO:6:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 917 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: DNA (genomic)
247
248 (ix) FEATURE:
249 (A) NAME/KEY: CDS
250 (B) LOCATION: 3..911
251
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
253
254 CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC 47
255 Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
256 1 5 10 15
257
258 ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC 95
    
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SEQUENCE VERIFICATION REPORT
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